

## SEQUENCE LISTINGS

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

NAME: ALLELIX BIOPHARMACEUTICALS INC.  
STREET: 6850 Goreway Drive  
CITY: Mississauga  
PROVINCE: Ontario  
COUNTRY: Canada  
POSTAL CODE: L4V 1V7  
TELEPHONE: (905) 677-0831  
FACSIMILE: (905) 677-9595

(ii) TITLE OF INVENTION: MAMMALIAN EDG-5 RECEPTOR HOMOLOGS

(iii) NUMBER OF SEQUENCES: 15

## (iv) CORRESPONDENCE ADDRESS:

(A) NAME: Orange Chari Pillay  
(B) STREET: Suite 3600, P.O. Box 190  
Toronto Dominion Bank Tower  
Toronto-Dominion Centre  
(C) CITY: Toronto  
(D) PROVINCE: Ontario  
(E) COUNTRY: Canada  
(F) ZIP: M5K 1H6

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: DOS EDITOR

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/CA98/01193  
(B) FILING DATE: 24-DEC-1998  
(C) CLASSIFICATION:

## (vi) PRIOR APPLICATION DATA:

(A) COUNTRY: U.S.A.  
(B) APPLICATION NUMBER: 08/997,803  
(C) FILING DATE: 24-DEC-1997  
(D) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Santosh K. Chari  
(B) FIRM: Orange Chari Pillay  
(C) REFERENCE NUMBER: 8700213-0006  
(D) TELEPHONE: (416) 868-3457  
(E) FACSIMILE: (416) 364-7910

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## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAAYTRSATMT STAAYYTGC G TGCGA

25

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified Site  
(B) LOCATION:4  
(D) OTHER INFORMATION: N is Inosine

(ix) FEATURE:

- (A) NAME/KEY: Modified Site  
(B) LOCATION:13  
(D) OTHER INFORMATION: N is Inosine

(ix) FEATURE:

- (A) NAME/KEY: Modified Site  
(B) LOCATION:16  
(D) OTHER INFORMATION: N is Inosine

(ix) FEATURE:

- (A) NAME/KEY: Modified Site  
(B) LOCATION:22  
(D) OTHER INFORMATION: N is Inosine

(ix) FEATURE:

- (A) NAME/KEY: Modified Site  
(B) LOCATION:25  
(D) OTHER INFORMATION: N is Inosine

(ix) FEATURE:

- (A) NAME/KEY: Modified Site  
(B) LOCATION:28  
(D) OTHER INFORMATION: N is Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTGNYKWTTTC ATNAWNMMRT ANAYNAYNGG RTT

33

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## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..634

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAC ACT GGC CCG GTG TCG AAA ACG TTG ACC GTC AAC CGC TGG TTC CTC	48
Asn Thr Gly Pro Val Ser Lys Thr Leu Thr Val Asn Arg Trp Phe Leu	
1 5 10 15	
CGC CAG GGG CTC CTA GAC ACC AGC CTG ACT GCC TCC CTG GCC AAT TTG	96
Arg Gln Gly Leu Leu Asp Thr Ser Leu Thr Ala Ser Leu Ala Asn Leu	
20 25 30	
CTG GTT ATT GCT GTG GAA AGA CAC ATG TCN ATC ATG AGG ATG AGA GTC	144
Leu Val Ile Ala Val Glu Arg His Met Ser Ile Met Arg Met Arg Val	
35 40 45	
CAC AGC AAC TTG ACC AAA AAG CGG GTG ACG CTG CTC ATT CTG CTG GTG	192
His Ser Asn Leu Thr Lys Lys Arg Val Thr Leu Leu Ile Leu Leu Val	
50 55 60	
TGG GCC ATC GCC ATC TTC ATG GGG GCC GTC CCC ACN CTG GGA TGG AAT	240
Trp Ala Ile Ala Ile Phe Met Gly Ala Val Pro Thr Leu Gly Trp Asn	
65 70 75 80	
TGC CTC TGC AAC ATC TCG GCC TGC TCT TCT CTG GCT CCC ATT TAC AGT	288
Cys Leu Cys Asn Ile Ser Ala Cys Ser Ser Leu Ala Pro Ile Tyr Ser	
85 90 95	
AGG AGT TAC CTC ATT TTC TGG ACT GTG TCC AAC CTC CTG GCC TTC TTC	336
Arg Ser Tyr Leu Ile Phe Trp Thr Val Ser Asn Leu Leu Ala Phe Phe	
100 105 110	
ATC ATG GTG GCG GTA TAC GTA CGC ATC TAC ATG TAT GTT AAA AGG AAA	384
Ile Met Val Ala Val Tyr Val Arg Ile Tyr Met Tyr Val Lys Arg Lys	
115 120 125	
ACC AAC GTC TTA TCT CCA CAC ACC AGT GGC TCC ATC AGC CGC CGG AGG	432
Thr Asn Val Leu Ser Pro His Thr Ser Gly Ser Ile Ser Arg Arg Arg	
130 135 140	
GCT CCC ATG AAG CTA ATG AAG ACA GTG ATG ACC GTC TTA GGC GCC TTC	480
Ala Pro Met Lys Leu Met Lys Thr Val Met Thr Val Leu Gly Ala Phe	
145 150 155 160	
GTG GTG TGC TGG ACC CCG GGT CTG GTG GTT CTG CTG CTG GAC GGC CTG	528
Val Val Cys Trp Thr Pro Gly Leu Val Val Leu Leu Leu Asp Gly Leu	
165 170 175	

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AAC TGC AAG CAG TGT AAC GTG CAA CAC GTG AAG NGC TGG TTC CTG CTG 576  
 Asn Cys Lys Gln Cys Asn Val Gln His Val Lys Xaa Trp Phe Leu Leu  
 180 185 190  
 CTC GCA CTG CTC AAC TCC GTC ATG AAC CCC CTC ATC TAC TGC CGC TCT 624  
 Leu Ala Leu Leu Asn Ser Val Met Asn Pro Leu Ile Tyr Cys Arg Ser  
 195 200 205  
 CCN NAC TTT CCA TGG 639  
 Pro Xaa Phe Pro Trp  
 210

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTTTACTCG AGATTGCTG GTTATTGCTG TGGAAAG 37

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTTCTAG ACGGTCATCA CTGTCTTCAT TAGCTTC 37

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGCGGCTGC ATAGCAACCT GACCAAAAAG 30

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## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATCCGCAGGT ACACCACAAC CATGATGAGG

30

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTTGTAGCAA GTTCAGCCTG GTTAAGT

27

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGGCTTATGA GTATTTCTTC CAGGGTA

27

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGTAGTCGG TACCTCTAGA GCAAGTTCAG CC

32

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

31

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1523 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 261..1322

(ix) FEATURE:

(A) NAME/KEY: Termination codon  
(B) LOCATION: 1320..1322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACCTTCCTA	ACCTGAGCGG	CCTAGCCTGG	GAAACAAACA	ATTAAATGT	GCGCTAAATG	60
CTGTGGTAGG	AGGTCAGGGG	CTATGTCCTG	GACCAAAGGA	CATTTGCACT	GAGACCTGAC	120
ACTTCAGGTC	TTCAACTCCC	TTGATGGGAG	TTAGCCAGAA	CGGGCTTAGA	AACAGCAATT	180
GATGGCTTAG	TGACTGATTT	TACAAATGAT	ATTTGTTTCT	TCTTTAAATT	TCTTTCTAGG	240
ATGTTCACTT	CTTCTCCACA	ATG AAT GAG	TGT CAC TAT	GAC AAG CAC	ATG	290
		Met Asn Glu	Cys His Tyr	Asp Lys His	Met	
		215		220		
GAC TTT TTT	TAT AAT AGG	AGC AAC ACT	GAT ACT GTC	GAT GAC TGG	ACA	338
Asp Phe Phe	Tyr Asn Arg	Ser Asn Thr	Asp Thr Val	Asp Asp Trp	Thr	
	225	230		235		
GGA ACA AAG	CTT GTG ATT	GTT TTG TGT	GTT GGG ACG	TTT TTC TGC	CTG	386
Gly Thr Lys	Leu Val Ile	Val Leu Cys	Val Gly Thr	Phe Phe Cys	Leu	
	240	245		250		
TTT ATT TTT	TTT TCT AAT	TCT CTG GTC	ATC GCG GCA	GTG ATC AAA	AAC	434

Phe Ile Phe Phe Ser Asn Ser Leu Val Ile Ala Ala Val Ile Lys Asn  
 255 260 265  
 AGA AAA TTT CAT TTC CCC TTT TAC TAC CTG TTG GCT AAT TTA GCT GCT 482  
 Arg Lys Phe His Phe Pro Phe Tyr Tyr Leu Leu Ala Asn Leu Ala Ala  
 270 275 280 285  
 GCC GAT TTC TTC GCT GGA ATT GCC TAT GTA TTC CTG ATG TTT AAC ACA 530  
 Ala Asp Phe Phe Ala Gly Ile Ala Tyr Val Phe Leu Met Phe Asn Thr  
 290 295 300  
 GGC CCA GTT TCA AAA ACT TTG ACT GTC AAC CGC TGG TTT CTC CGT CAG 578  
 Gly Pro Val Ser Lys Thr Leu Thr Val Asn Arg Trp Phe Leu Arg Gln  
 305 310 315  
 GGG CTT CTG GAC AGT AGC TTG ACT GCT TCC CTC ACC AAC TTG CTG GTT 626  
 Gly Leu Leu Asp Ser Ser Leu Thr Ala Ser Leu Thr Asn Leu Leu Val  
 320 325 330  
 ATC GCC GTG GAG AGG CAC ATG TCA ATC ATG AGG ATG CGG GTC CAT AGC 674  
 Ile Ala Val Glu Arg His Met Ser Ile Met Arg Met Arg Val His Ser  
 335 340 345  
 AAC CTG ACC AAA AAG AGG GTG ACA CTG CTC ATT TTG CTT GTC TGG GCC 722  
 Asn Leu Thr Lys Lys Arg Val Thr Leu Leu Ile Leu Leu Val Trp Ala  
 350 355 360 365  
 ATC GCC ATT TTT ATG GGG GCG GTC CCC ACA CTG GGC TGG AAT TGC CTC 770  
 Ile Ala Ile Phe Met Gly Ala Val Pro Thr Leu Gly Trp Asn Cys Leu  
 370 375 380  
 TGC AAC ATC TCT GCC TGC TCT TCC CTG GCC CCC ATT TAC AGC AGG AGT 818  
 Cys Asn Ile Ser Ala Cys Ser Ser Leu Ala Pro Ile Tyr Ser Arg Ser  
 385 390 395  
 TAC CTT GTT TTC TGG ACA GTG TCC AAC CTC ATG GCC TTC CTC ATC ATG 866  
 Tyr Leu Val Phe Trp Thr Val Ser Asn Leu Met Ala Phe Leu Ile Met  
 400 405 410  
 GTT GTG GTG TAC CTG CGG ATC TAC GTG TAC GTC AAG AGG AAA ACC AAC 914  
 Val Val Val Tyr Leu Arg Ile Tyr Val Tyr Val Lys Arg Lys Thr Asn  
 415 420 425  
 GTC TTG TCT CCG CAT ACA AGT GGG TCC ATC AGC CGC CGG AGG ACA CCC 962  
 Val Leu Ser Pro His Thr Ser Gly Ser Ile Ser Arg Arg Arg Thr Pro  
 430 435 440 445  
 ATG AAG CTA ATG AAG ACG GTG ATG ACT GTC TTA GGG GCG TTT GTG GTA 1010  
 Met Lys Leu Met Lys Thr Val Met Thr Val Leu Gly Ala Phe Val Val  
 450 455 460  
 TGC TGG ACC CCG GGC CTG GTG GTT CTG CCC CTC GAC GGC CTG AAC TGC 1058  
 Cys Trp Thr Pro Gly Leu Val Val Leu Pro Leu Asp Gly Leu Asn Cys  
 465 470 475  
 AGG CAG TGT GGC GTG CAG CAT GTG AAA AGG TGG TTC CTG CTG CTG GCG 1106  
 Arg Gln Cys Gly Val Gln His Val Lys Arg Trp Phe Leu Leu Leu Ala  
 480 485 490  
 CTG CTC AAC TCC GTC GTG AAC CCC ATC ATC TAC TCC TAC AAG GAC GAG 1154  
 Leu Leu Asn Ser Val Val Asn Pro Ile Ile Tyr Ser Tyr Lys Asp Glu

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495 500 505

GAC ATG TAT GGC ACC ATG AAG AAG ATG ATC TGC TGC TTC TCT CAG GAG 1202  
 Asp Met Tyr Gly Thr Met Lys Lys Met Ile Cys Cys Phe Ser Gln Glu  
 510 515 520 525

AAC CCA GAG AGG CGT CCC TCT CGC ATC CCC TCC ACA GTC CTC AGC AGG 1250  
 Asn Pro Glu Arg Arg Pro Ser Arg Ile Pro Ser Thr Val Leu Ser Arg  
 530 535 540

AGT GAC ACA GGC AGC CAG TAC ATA GAG GAT AGT ATT AGC CAA GGT GCA 1298  
 Ser Asp Thr Gly Ser Gln Tyr Ile Glu Asp Ser Ile Ser Gln Gly Ala  
 545 550 555

GTC TGC AAT AAA AGC ACT TCC TAA ACTCTGGATG CCTCTYGGCC CACCCAGGCC 1352  
 Val Cys Asn Lys Ser Thr Ser  
 560 565

TCCTCTGGGA AAAGAGCTGT TAAGAATGAT TACCTGTCTC TAACAAAGCC CATGTACAGT 1412

GTTATTTGAG GTCTCCATTA ATCACTGCTA GATTTCTTTA AAAAATTTTT TTTCATAGTT 1472

TAAAAGCATG GGCAGTAAAG AGAGGACCTG CTGCATTTAG AGAAAGCACA G 1523

## (2) INFORMATION FOR SEQ ID NO:13

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1356 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

GAATTCGCGG CCGCGTCGAC GTTCACTTCT CCACAATGAA TGAGTGTAC TATGACAAGC 60

ACATGGACTT TTTTATAAT AGGAGCAACA CTGATACTGT CGATGACTGG ACAGGAACAA 120

AGCTTGTGAT TGTTTTGTGT GTTGGGACGT TTTTCTCCCT GTTTATTTTT TTTTCTAATT 180

CTCTGGTCAT CGCGGCAGTG ATCAAAAACA GAAAATTTCA TTTCCCCTTT TACTACCTGT 240

TGGCTAATTT AGCTGCTGCC GATTTCTTCG CTGGAATTGG CTATGTATTC CTGATGTTTA 300

ACACAGGCCC AGTTTCAAAA ACTTTGACTG TCAACCGCTG GTTTCTCCGT CAGGGGCTTC 360

TGGACAGTAG CTTGACTGCT TCCCTACCA ACTTGCTGGT TATCGCCGTG GAGAGGCACA 420

TGTCAATCAT GAGGATGCGG GTCCATAGCA ACCTGACCAA AAAGAGGGTG AACTGCTCA 480

TTTTGCTTGT CTGGGCCATC GCCATTTTTA TGGGGGCGGT CCCCACACTG GGCTGGAATT 540

GCCTCTGCAA CATCTCTGCC TGCTCTTCCC TGGCCCCCAT TTACAGCAGG AGTTACCTTG 600

TTTTCTGGAC AGTGTCCAAC CTCATGGCCT TCCTCATCAT GGTTGTGGTG TACCTGCGGA 660

TCTACGTGTA CGTCAAGAGG AAAACCAACG TCTTGTCTCC GCATACAAGT GGGTCCATCA 720

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GCCGCGGGAG GACACCCATG AAGCTAATGA AGACGGTGAT GACTGTCTTA GGGGCGTTTG 780  
 TGGTATGCTG GACCCCGGGC CTGGTGGTTC TGCCCCCTGA CGGCCTGAAC TGCAGGCAGT 840  
 GTGGCGTGCA GCATGTGAAA AGGTGGTTCC TGCTGCTGGC GCTGCTCAAC TCCGTCGTGA 900  
 ACCCCATCAT CTA CTCTCTAC AAGGACGAGG ACATGTATGG CACCATGAAG AAGATGATCT 960  
 GCTGCTTCTC TCAGGAGAAC CCAGAGAGGC GTCCCTCTCG CATCCCCCTCC ACAGTCCTCA 1020  
 GCAGGAGTGA CACAGGCAGC CAGTACATAG AGGATAGTAT TAGCCAAGGT GCAGTCTGCA 1080  
 ATAAAAGCAC TTCCTAAACT CTGGATGCCT CTGGCCCACC CAGGCCTCCT CTGGGAAAAG 1140  
 AGCTGTAAAG AATGATTACC TGTCTCTAAC AAAGCCCATG TACAGTGTTA TTTGAGGTCT 1200  
 CCATTAATCA CTGCTAGATT TCTTTAAAAA ATTTTTCCTC ATAGTTTAAA AGCATGGGCA 1260  
 GTAAAGAGAG GACCTGCTGC ATTTAGAGAA AGCACAGGTC GACGCGGCCG CGAATTCTTT 1320  
 TGCTTTTAC CCTGGAAGAA ATACTCGAGC ATGCAT 1356

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Asn Glu Cys His Tyr Asp Lys His Met Asp Phe Phe Tyr Asn Arg  
 1 5 10 15  
 Ser Asn Thr Asp Thr Val Asp Asp Trp Thr Gly Thr Lys Leu Val Ile  
 20 25 30  
 Val Leu Cys Val Gly Thr Phe Phe Cys Leu Phe Ile Phe Phe Ser Asn  
 35 40 45  
 Ser Leu Val Ile Ala Ala Val Ile Lys Asn Arg Lys Phe His Phe Pro  
 50 55 60  
 Phe Tyr Tyr Leu Leu Ala Asn Leu Ala Ala Asp Phe Phe Ala Gly  
 65 70 75 80  
 Ile Ala Tyr Val Phe Leu Met Phe Asn Thr Gly Pro Val Ser Lys Thr  
 85 90 95  
 Leu Thr Val Asn Arg Trp Phe Leu Arg Gln Gly Leu Leu Asp Ser Ser  
 100 105 110  
 Leu Thr Ala Ser Leu Thr Asn Leu Leu Val Ile Ala Val Glu Arg His  
 115 120 125  
 Met Ser Ile Met Arg Met Arg Val His Ser Asn Leu Thr Lys Lys Arg

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130 135 140

Val Thr Leu Leu Ile Leu Leu Val Trp Ala Ile Ala Ile Phe Met Gly  
145 150 155 160

Ala Val Pro Thr Leu Gly Trp Asn Cys Leu Cys Asn Ile Ser Ala Cys  
165 170 175

Ser Ser Leu Ala Pro Ile Tyr Ser Arg Ser Tyr Leu Val Phe Trp Thr  
180 185 190

Val Ser Asn Leu Met Ala Phe Leu Ile Met Val Val Val Tyr Leu Arg  
195 200 205

Ile Tyr Val Tyr Val Lys Arg Lys Thr Asn Val Leu Ser Pro His Thr  
210 215 220

Ser Gly Ser Ile Ser Arg Arg Arg Thr Pro Met Lys Leu Met Lys Thr  
225 230 235 240

Val Met Thr Val Leu Gly Ala Phe Val Val Cys Trp Thr Pro Gly Leu  
245 250 255

Val Val Leu Pro Leu Asp Gly Leu Asn Cys Arg Gln Cys Gly Val Gln  
260 265 270

His Val Lys Arg Trp Phe Leu Leu Leu Ala Leu Leu Asn Ser Val Val  
275 280 285

Asn Pro Ile Ile Tyr Ser Tyr Lys Asp Glu Asp Met Tyr Gly Thr Met  
290 295 300

Lys Lys Met Ile Cys Cys Phe Ser Gln Glu Asn Pro Glu Arg Arg Pro  
305 310 315 320

Ser Arg Ile Pro Ser Thr Val Leu Ser Arg Ser Asp Thr Gly Ser Gln  
325 330 335

Tyr Ile Glu Asp Ser Ile Ser Gln Gly Ala Val Cys Asn Lys Ser Thr  
340 345 350

Ser

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asn Thr Gly Pro Val Ser Lys Thr Leu Thr Val Asn Arg Trp Phe Leu  
1 5 10 15

Arg Gln Gly Leu Leu Asp Thr Ser Leu Thr Ala Ser Leu Ala Asn Leu

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20 25 30  
 Leu Val Ile Ala Val Glu Arg His Met Ser Ile Met Arg Met Arg Val  
 35 40 45  
 His Ser Asn Leu Thr Lys Lys Arg Val Thr Leu Leu Ile Leu Leu Val  
 50 55 60  
 Trp Ala Ile Ala Ile Phe Met Gly Ala Val Pro Thr Leu Gly Trp Asn  
 65 70 75 80  
 Cys Leu Cys Asn Ile Ser Ala Cys Ser Ser Leu Ala Pro Ile Tyr Ser  
 85 90 95  
 Arg Ser Tyr Leu Ile Phe Trp Thr Val Ser Asn Leu Leu Ala Phe Phe  
 100 105 110  
 Ile Met Val Ala Val Tyr Val Arg Ile Tyr Met Tyr Val Lys Arg Lys  
 115 120 125  
 Thr Asn Val Leu Ser Pro His Thr Ser Gly Ser Ile Ser Arg Arg Arg  
 130 135 140  
 Ala Pro Met Lys Leu Met Lys Thr Val Met Thr Val Leu Gly Ala Phe  
 145 150 155 160  
 Val Val Cys Trp Thr Pro Gly Leu Val Val Leu Leu Leu Asp Gly Leu  
 165 170 175  
 Asn Cys Lys Gln Cys Asn Val Gln His Val Lys Xaa Trp Phe Leu Leu  
 180 185 190  
 Leu Ala Leu Leu Asn Ser Val Met Asn Pro Leu Ile Tyr Cys Arg Ser  
 195 200 205  
 Pro Xaa Phe Pro Trp  
 210